



Figure S2. Overview of the quantitative phosphoproteomics analysis. Total proteins of 25 DAP seeds of HFA and LFA were extracted and digested by trypsin. Both peptide of HFA and LFA were labeled by Dimethyl and Dimethyl:2H(6), respectively. Dimethyl labeled HFA was mixed with Dimethyl:2H(6) labeled LFA at 1:1 as shown in purple (forward), and Dimethyl:2H(6) labeled HFA was mixed with Dimethyl labeled LFA at 1:1 as shown in blue (reciprocal). The data were quantified and put together to calculate the results using the software Silique-N (Alpharomics Co., Limited, Shenzhen, China). It is related to Fig 1 and Datasets S1-S4. HFA, a *Brassica napus* line with high seed oil content; LFA, a *Brassica napus* line with low seed oil content; DAP, day after pollination.